

WHAT IS CLAIMED IS:

1. A method of preparing a monocot plant other than *Coix* expressing a selected gene comprising the steps of:
 - (a) providing a selected gene;
 - 5 (b) preparing a construct comprising said gene operably linked to a *Coix* promoter;
 - (c) transforming a recipient cell from a monocot plant other than *Coix* with said construct; and
 - (d) regenerating a monocot plant which expresses said gene from said recipient cell.
- 10 2. The method of claim 1, wherein said monocot plant is a plant selected from the group consisting of rice, wheat, oats, barley, rye, sorghum and maize.
3. The method of claim 2, wherein the monocot plant is maize.
- 15 4. The method of claim 1, wherein said step of transforming comprises microprojectile bombardment, PEG mediated transformation of protoplasts, electroporation, silicon carbide fiber mediated transformation, or *Agrobacterium*-mediated transformation.
5. The method of claim 4, wherein said microprojectile bombardment comprises coating
20 microprojectiles with DNA comprising said construct and contacting said recipient cells with said microprojectiles.
6. The method of claim 1, wherein said selected gene comprises a gene selected from the group consisting of an insect resistance gene, a fungal disease resistance gene, a viral disease
25 resistance gene, a bacterial disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker gene, a gene affecting plant agronomic characteristics, and an environment or stress resistance gene.

7. The method of claim 1, wherein said *Coix* promoter is a promoter from a *Coix* gene homologous to a gene selected from the group consisting of gamma zein, oleosin ole16, globulin1, actin1, actin c1, sucrose synthetase, INOPS, EMB5, globulin2, b-32, ADPG-pyrophosphorylase, Ltp1, Ltp2, oleosin ole17, oleosin ole18, actin2, pollen-specific protein, pollen-specific pectate lyase, anther-specific protein, anther-specific gene RTS2, pollen-specific gene, tapetum-specific gene, tapetum-specific gene RAB24, anthranilate synthase alpha subunit, alpha zein, anthranilate synthase beta subunit, dihydrodipicolinate synthase, Thi1, alcohol dehydrogenase, cab binding protein, H3C4, RUBISCO SS starch branching enzyme, ACCase, actin3, actin7, regulatory protein GF`14-12, ribosomal protein L9, cellulose biosynthetic enzyme, S-adenosyl-L-homocysteine hydrolase, superoxide dismutase, C-kinase receptor, phosphoglycerate mutase, root-specific RCc3 mRNA, glucose-6 phosphate isomerase, pyrophosphate-fructose 6-phosphate1phosphotransferase, ubiquitin, beta-ketoacyl-ACP synthase, 33kDa photosystem II, oxygen evolving protein, 69 kDa vacuolar ATPase subunit, metallothionein-like protein, glyceraldehyde-3-phosphate dehydrogenase, ABA- and ripening-inducible-like protein, phenylalanine ammonia lyase, adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase, α -tubulin, cab, PEPCase, R, lectin, light harvesting complex, heat shock protein, chalcone synthase, zein, globulin-1, ABA, auxin-binding protein, UDP glucose flavonoid glycosyl-transferase gene, MPI, actin, opaque 2, b70, and oleosin.

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8. The method of claim 1, wherein said *Coix* promoter is a gamma coixin promoter.

9. A method of producing progeny comprising the steps of:

- (a) preparing a monocot plant according to the method of claim 1; and
- (b) crossing said plant with a second plant or with itself.

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10. A method of plant breeding comprising the steps of:

- (a) obtaining a progeny plant according to the method of claim 9; and
- (b) crossing said plant with itself or a second plant.

11. A method of preventing gene silencing in a monocot plant other than *Coix* comprising the steps of:

- (a) providing a *Coix* promoter;
- 5 (b) preparing a construct comprising said *Coix* promoter operably linked to a selected gene;
- (d) transforming a recipient cell from a monocot plant other than *Coix* with said construct; and
- 10 (e) regenerating a plant expressing said gene from said recipient cell, whereby said plant does not exhibit gene silencing.

12. The method of claim 11, wherein the monocot is selected from the group consisting of rice, wheat, barley, rye, oats, sorghum and maize.

13. The method of claim 12, wherein the monocot is maize.

14. The method of claim 11, wherein said step of transforming comprises microprojectile bombardment, PEG mediated transformation of protoplasts, electroporation, silicon carbide fiber mediated transformation, or *Agrobacterium*-mediated transformation.

15. The method of claim 14, wherein said microprojectile bombardment comprises coating microprojectiles with DNA comprising said construct and contacting said recipient cells with said microprojectiles.

16. The method of claim 11, wherein said selected gene is an insect resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a bacterial disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable

marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, or an environment or stress resistance gene.

17. The method of claim 11, wherein said *Coix* promoter is a promoter from a *Coix* gene
5 homologous to a gene from a monocot other than *Coix* selected from the group consisting of
gamma zein, oleosin ole16, globulin1, actin1, actin c1, sucrose synthetase, INOPS, EMB5,
globulin2, b-32, ADPG-pyrophosphorylase, Ltp1, Ltp2, oleosin ole17, oleosin ole18, actin2,
pollen-specific protein, pollen-specific pectate lyase, anther-specific protein, anther-specific gene
RTS2, pollen-specific gene, tapetum-specific gene, tapetum-specific gene RAB24, anthranilate
10 synthase alpha subunit, alpha zein, anthranilate synthase beta subunit, dihydrodipicolinate
synthase, Thi1, alcohol dehydrogenase, cab binding protein, H3C4, RUBISCO SS starch
branching enzyme, ACCase, actin3, actin7, regulatory protein GF'14-12, ribosomal protein L9,
cellulose biosynthetic enzyme, S-adenosyl-L-homocysteine hydrolase, superoxide dismutase, C-
kinase receptor, phosphoglycerate mutase, root-specific RCc3 mRNA, glucose-6 phosphate
15 isomerase, pyrophosphate-fructose 6-phosphate1phosphotransferase, ubiquitin, beta-ketoacyl-
ACP synthase, 33kDa photosystem II, oxygen evolving protein, 69 kDa vacuolar ATPase
subunit, metallothionein-like protein, glyceraldehyde-3-phosphate dehydrogenase, ABA- and
ripening-inducible-like protein, phenylalanine ammonia lyase, adenosine triphosphatase S-
adenosyl-L-homocysteine hydrolase, α -tubulin, cab, PEPCase, R, lectin, light harvesting
20 complex, heat shock protein, chalcone synthase, zein, globulin-1, ABA, auxin-binding protein,
UDP glucose flavonoid glycosyl-transferase gene, MPI, actin, opaque 2, b70, and oleosin.

18. The method of claim 17, wherein the step of providing comprises hybridization of DNA
from a gene of a monocot species other than *Coix* or flanking sequences thereof to DNA from
25 *Coix*.

19. The method of claim 18, wherein said monocot species other than *Coix* and said monocot
plant other than *Coix* are members of the same species.

20. The method of claim 18, wherein said DNA from *Coix* comprises a library of genomic DNA clones.

21. The method of claim 11, wherein the step of providing a *Coix* promoter comprises PCR™.

22. A method of producing progeny comprising the steps of:
(a) preparing a plant according to the method of claim 11; and
(b) crossing said plant with a second plant or with itself.

23. A method of plant breeding comprising the steps of:
(a) obtaining a progeny plant according to the method of claim 22, wherein said progeny plant comprises said construct; and
(b) crossing said plant with itself or a second plant.

24. A method of preparing a monocot expression vector comprising
(a) identifying a first promoter from a monocot other than *Coix* having a desirable expression profile;
(b) isolating a *Coix* promoter that is homologous to said first promoter; and
(c) constructing an expression vector comprising said *Coix* promoter operably linked to a selected gene.

25. The method of claim 24, wherein the monocot is selected from the group consisting of rice, wheat, barley, rye, sorghum, oats and maize.

26. The method of claim 25, wherein the monocot is maize.

27. The method of claim 24, wherein said selected gene encodes a trait selected from the group consisting of an insect resistance gene, a fungal disease resistance gene, a viral disease

resistance gene, a bacterial disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, and an environment or stress resistance gene.

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28. The method of claim 24, wherein said monocot promoter is from a gene selected from the group consisting of gamma zein, oleosin ole16, globulin1, actin1, actin c1, sucrose synthetase, INOPS, EMB5, globulin2, b-32, ADPG-pyrophosphorylase, Ltp1, Ltp2, oleosin ole17, oleosin ole18, actin2, pollen-specific protein, pollen-specific pectate lyase, anther-specific protein, 10 anther-specific gene RTS2, pollen-specific gene, tapetum-specific gene, tapetum-specific gene RAB24, anthranilate synthase alpha subunit, alpha zein, anthranilate synthase beta subunit, dihydrodipicolinate synthase, Thi1, alcohol dehydrogenase, cab binding protein, H3C4, RUBISCO SS starch branching enzyme, ACCase, actin3, actin7, regulatory protein GF'14-12, ribosomal protein L9, cellulose biosynthetic enzyme, S-adenosyl-L-homocysteine hydrolase, 15 superoxide dismutase, C-kinase receptor, phosphoglycerate mutase, root-specific RCc3 mRNA, glucose-6 phosphate isomerase, pyrophosphate-fructose 6-phosphate1phosphotransferase, ubiquitin, beta-ketoacyl-ACP synthase, 33kDa photosystem II, oxygen evolving protein, 69 kDa vacuolar ATPase subunit, metallothionein-like protein, glyceraldehyde-3-phosphate dehydrogenase, ABA- and ripening-inducible-like protein, phenylalanine ammonia lyase, 20 adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase, α -tubulin, cab, PEPCase, R, lectin, light harvesting complex, heat shock protein, chalcone synthase, zein, globulin-1, ABA, auxin-binding protein, UDP glucose flavonoid glycosyl-transferase gene, MPI, actin, opaque 2, b70, and oleosin.

25 29. The method of claim 28, wherein the step of identifying comprises hybridization of DNA from said monocot gene or flanking sequences thereof to DNA from *Coix*.

30. The method of claim 29, wherein said DNA from *Coix* comprises a library of genomic DNA clones.

31. The method of claim 28, wherein the step of identifying a *Coix* promoter comprises PCR™.

5 32. An isolated gamma coixin promoter isolatable from the nucleic acid sequence of SEQ ID NO:8.

33. An isolated nucleic acid sequence comprising from about 80 to about 894 contiguous nucleotides of SEQ ID NO:8.

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34. The isolated nucleic acid sequence of claim 33, comprising from about 222 to about 894 contiguous nucleotides of SEQ ID NO:8.

15 35. The isolated nucleic acid sequence of claim 34, comprising the nucleic acid sequence of SEQ ID NO:18.

36. The isolated nucleic acid sequence of claim 35, comprising from about 412 to about 894 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:8.

20 37. The isolated nucleic acid sequence of claim 36, comprising the nucleic acid sequence of SEQ ID NO:19.

38. An isolated gamma coixin terminator isolatable from the nucleic acid sequence of SEQ ID NO:11.

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39. A nucleic acid sequence comprising from about 80 to about 412 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:11.

40. The nucleic acid sequence of claim 39, comprising from about 200 to about 412

contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:11.

41. The nucleic acid sequence of claim 40, comprising from about 325 to about 412 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:11.

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42. The nucleic acid sequence of claim 41, comprising the nucleic acid sequence of SEQ ID NO:11.

43. A *Coix* oleosin 3 terminator isolatable from the nucleic acid sequence of SEQ ID NO:17.

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44. An isolated nucleic acid sequence comprising from about 50 to about 377 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:17.

45. The isolated nucleic acid sequence of claim 44, comprising from about 120 to about 377 contiguous nucleotides of the nucleic acid sequence SEQ ID NO:17.

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46. The isolated nucleic acid sequence of claim 45, comprising from about 220 to about 377 contiguous nucleotides of the nucleic acid sequence SEQ ID NO:17.

47. The isolated nucleic acid sequence of claim 46, comprising from about 300 to about 377 contiguous nucleotides of the nucleic acid sequence SEQ ID NO:17.

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48. The isolated nucleic acid sequence of claim 47, comprising the nucleic acid sequence SEQ ID NO:17.

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49. A fertile transgenic plant comprising a selected DNA, said selected DNA comprising a gamma coixin promoter.

50. The plant of claim 49, wherein said promoter comprises a nucleic acid sequence selected from the group consisting of the nucleic acid sequence of claim 32, the nucleic acid sequence of claim 33, the nucleic acid sequence of claim 34, the nucleic acid sequence of claim 35, and the nucleic acid sequence of claim 36.

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51. The plant of claim 50, wherein said promoter is operably linked to an exogenous gene selected from the group consisting of an insect resistance gene, a disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, and an environment or stress resistance gene.

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52. A fertile transgenic plant comprising a selected DNA, said selected DNA comprising a gene encoding gamma coixin operably linked to a promoter which is not native to said gamma coixin gene.

53. The fertile transgenic plant of claim 52, wherein said gene encoding gamma coixin encodes the polypeptide encoded by the nucleic acid sequence of SEQ ID NO:16.

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54. A fertile transgenic plant comprising a selected DNA, said selected DNA comprising a gamma coixin terminator.

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55. The fertile transgenic plant of claim 54, wherein said gamma coixin terminator comprises a nucleic acid sequence selected from the group consisting of the nucleic acid sequence of claim 39, the nucleic acid sequence of claim 40, the nucleic acid sequence of claim 41, and the nucleic acid sequence of claim 42.

56. A fertile transgenic plant comprising a selected DNA, said selected DNA comprising a *Coix* oleosin 3 terminator.

57. The fertile transgenic plant of claim 56, wherein said *Coix* oleosin 3 terminator comprises a nucleic acid sequence selected from the group consisting of the nucleic acid sequence of claim 44, the nucleic acid sequence of claim 45, the nucleic acid sequence of claim 46, the nucleic acid sequence of claim 47, and the nucleic acid sequence of claim 48.

58. A progeny plant of any generation of the plant of claim 49, 52, 54 or 56, wherein said progeny plant comprises said selected DNA.

59. The fertile transgenic plant of claim 49, 52, 54 or 56, wherein said plant is a monocot plant selected from the group consisting of rice, wheat, barley, rye, sorghum and maize.

60. The fertile transgenic plant of claim 59, wherein the monocot is maize.

61. The fertile transgenic plant of claim 49, 52, 54, or 56 wherein said plant is a dicot plant selected from the group consisting of tobacco, tomato, potato, soybean and cotton.

62. A method of plant breeding comprising crossing the fertile transgenic plant of claim 49, 52, 54 or 56, or a transgenic progeny thereof, with itself or a second plant.

63. An isolated nucleic acid sequence encoding a *Coix* gene selected from the group consisting of oleosin ole16, globulin1, actin1, actin c1, sucrose synthetase, INOPS, EMB5, globulin2, b-32, ADPG-pyrophosphorylase, Ltp1, Ltp2, oleosin ole17, oleosin ole18, actin2, pollen-specific protein, pollen-specific pectate lyase, anther-specific protein, anther-specific gene RTS2, pollen-specific gene, tapetum-specific gene, tapetum-specific gene RAB24, anthranilate synthase alpha subunit, alpha zein, anthranilate synthase beta subunit, dihydrodipicolinate synthase, Thi1, alcohol dehydrogenase, cab binding protein, H3C4, RUBISCO SS starch branching enzyme, ACCase, actin3, actin7, regulatory protein GF'14-12, ribosomal protein L9, cellulose biosynthetic enzyme, S-adenosyl-L-homocysteine hydrolase, superoxide dismutase, C-

kinase receptor, phosphoglycerate mutase, root-specific RCc3 mRNA, glucose-6 phosphate isomerase, pyrophosphate-fructose 6-phosphate1phosphotransferase, ubiquitin, beta-ketoacyl-ACP synthase, 33kDa photosystem II, oxygen evolving protein, 69 kDa vacuolar ATPase subunit, metallothionein-like protein, glyceraldehyde-3-phosphate dehydrogenase, ABA- and
5 ripening-inducible-like protein, phenylalanine ammonia lyase, adenosine triphosphatase S-adenosyl-L-homocysteine hydrolase, α -tubulin, cab, PEPCase, R, lectin, light harvesting complex, heat shock protein, chalcone synthase, zein, globulin-1, ABA, auxin-binding protein, UDP glucose flavonoid glycosyl-transferase gene, MPI, oleosin, actin, opaque 2, and b70.